

SEQUENCE PROTOCOL

<110> Degussa-Hüls AG

5 <120> Process for the fermentative preparation of
L-amino acids using strains of the
Enterobacteriaceae family.

<130> 000613 BT

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<140>

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<170> PatentIn Ver. 2.1

<210> 1

<211> 1719

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<212> DNA

<213> *Escherichia coli*

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<221> CDS

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<222> (1) .. (1716)

<223> poxB

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ggg gtg aaa cgc atc tgg gga gtc aca ggc gac tct ctg aac ggt ctt 96
Gly Val Lys Arg Ile Trp Gly Val Thr Gly Asp Ser Leu Asn Gly Leu
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40

agt gac agt ctt aat cgc atg ggc acc atc gag tgg atg tcc acc cgc 144
Ser Asp Ser Leu Asn Arg Met Gly Thr Ile Glu Trp Met Ser Thr Arg
35 40 45

cac gaa gaa gtg gcg gcc ttt gcc gct ggc gct gaa gca caa ctt agc 192
His Glu Glu Val Ala Ala Phe Ala Ala Gly Ala Glu Ala Gln Leu Ser
50 55 60

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5	tta atc aac ggc ctg ttc gat tgc cac cgc aat cac gtt ccg gta ctg	288
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	gcg att gcc gct cat att ccc tcc agc gaa att ggc agc ggc tat ttc	336
10	Ala Ile Ala Ala His Ile Pro Ser Ser Glu Ile Gly Ser Gly Tyr Phe	
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	cag gaa acc cac cca caa gag cta ttc cgc gaa tgt agt cac tat tgc	384
	Gln Glu Thr His Pro Gln Glu Leu Phe Arg Glu Cys Ser His Tyr Cys	
15	115 120 125	
	gag ctg gtt tcc agc ccg gag cag atc cca caa gta ctg gcg att gcc	432
	Glu Leu Val Ser Ser Pro Glu Gln Ile Pro Gln Val Leu Ala Ile Ala	
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	atg cgc aaa gcg gtg ctt aac cgt ggc gtt tgc gtt gtc gtg tta cca	480
	Met Arg Lys Ala Val Leu Asn Arg Gly Val Ser Val Val Val Leu Pro	
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25	ggc gac gtg gcg tta aaa cct gcg cca gaa ggg gca acc atg cac tgg	528
	Gly Asp Val Ala Leu Lys Pro Ala Pro Glu Gly Ala Thr Met His Trp	
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	tat cat gcg cca caa cca gtc gtg acg ccg gaa gaa gaa gag tta cgc	576
30	Tyr His Ala Pro Gln Pro Val Val Thr Pro Glu Glu Glu Glu Leu Arg	
	180 185 190	
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	Lys Leu Ala Gln Leu Leu Arg Tyr Ser Ser Asn Ile Ala Leu Met Cys	
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	ggc agc ggc tgc gcg ggg gcg cat aaa gag tta gtt gag ttt gcc ggg	672
	Gly Ser Gly Cys Ala Gly Ala His Lys Glu Leu Val Glu Phe Ala Gly	
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40	aaa att aaa gcg cct att gtt cat gcc ctg cgc ggt aaa gaa cat gtc	720
	Lys Ile Lys Ala Pro Ile Val His Ala Leu Arg Gly Lys Glu His Val	
	225 230 235 240	

10076416-01902

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	Glu Tyr Asp Asn Pro Tyr Asp Val Gly Met Thr Gly Leu Ile Gly Phe	
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5	tcg tca ggt ttc cat acc atg atg aac gcc gac acg tta gtg cta ctc	816
	Ser Ser Gly Phe His Thr Met Met Asn Ala Asp Thr Leu Val Leu Leu	
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	ggc acg caa ttt ccc tac cgc gcc ttc tac ccg acc gat gcc aaa atc	864
10	Gly Thr Gln Phe Pro Tyr Arg Ala Phe Tyr Pro Thr Asp Ala Lys Ile	
	275 280 285	
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	gat atg gca ctg gtc ggc gat atc aag tcg act ctg cgt gca ttg ctt	960
	Asp Met Ala Leu Val Gly Asp Ile Lys Ser Thr Leu Arg Ala Leu Leu	
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20	cca ttg gtg gaa gaa aaa gcc gat cgc aag ttt ctg gat aaa gcg ctg	1008
	Pro Leu Val Glu Glu Lys Ala Asp Arg Lys Phe Leu Asp Lys Ala Leu	
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25	gaa gat tac cgc gac gcc cgc aaa ggg ctg gac gat tta gct aaa ccg	1056
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	Phe Ala Ala Asp Asp Ala Ile Phe Thr Cys Asp Val Gly Thr Pro Thr	
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	Val Trp Ala Ala Arg Tyr Leu Lys Met Asn Gly Lys Arg Arg Leu Leu	
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Gly Ala Gln Ala Thr Glu Pro Glu Arg Gln Val Val Ala Met Cys Gly
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5 gat ggc ggt ttt agc atg ttg atg ggc gat ttc ctc tca gta gtg cag 1344
Asp Gly Gly Phe Ser Met Leu Met Gly Asp Phe Leu Ser Val Val Gln
435 440 445

10 atg aaa ctg cca gtg aaa att gtc gtc ttt aac aac agc gtg ctg ggc 1392
Met Lys Leu Pro Val Lys Ile Val Val Phe Asn Asn Ser Val Leu Gly
450 455 460

15 ttt gtg gcg atg gag atg aaa gct ggt ggc tat ttg act gac ggc acc 1440
Phe Val Ala Met Glu Met Lys Ala Gly Gly Tyr Leu Thr Asp Gly Thr
465 470 475 480

20 gaa cta cac gac aca aac ttt gcc cgc att gcc gaa gcg tgc ggc att 1488
Glu Leu His Asp Thr Asn Phe Ala Arg Ile Ala Glu Ala Cys Gly Ile
485 490 495

25 acg ggt atc cgt gta gaa aaa gcg tct gaa gtt gat gaa gcc ctg caa 1536
Thr Gly Ile Arg Val Glu Lys Ala Ser Glu Val Asp Glu Ala Leu Gln
500 505 510

30 cgc gcc ttc tcc atc gac ggt ccg gtg ttg gtg gat gtg gtg gtc gcc 1584
Arg Ala Phe Ser Ile Asp Gly Pro Val Leu Val Asp Val Val Val Ala
515 520 525

35 aaa gaa gag tta gcc att cca ccg cag atc aaa ctc gaa cag gcc aaa 1632
Lys Glu Glu Leu Ala Ile Pro Pro Gln Ile Lys Leu Glu Gln Ala Lys
530 535 540

40 ggt ttc agc ctg tat atg ctg cgc gca atc atc agc gga cgc ggt gat 1680
Gly Phe Ser Leu Tyr Met Leu Arg Ala Ile Ile Ser Gly Arg Gly Asp
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gaa gtg atc gaa ctg gcg aaa aca aac tgg cta agg taa 1719
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<211> 572
<212> PRT

<213> Escherichia coli

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10 Ser Asp Ser Leu Asn Arg Met Gly Thr Ile Glu Trp Met Ser Thr Arg
35 40 45

His Glu Glu Val Ala Ala Phe Ala Ala Gly Ala Glu Ala Gln Leu Ser
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15 Gly Glu Leu Ala Val Cys Ala Gly Ser Cys Gly Pro Gly Asn Leu His
65 70 75 80

20 Leu Ile Asn Gly Leu Phe Asp Cys His Arg Asn His Val Pro Val Leu
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Ala Ile Ala Ala His Ile Pro Ser Ser Glu Ile Gly Ser Gly Tyr Phe
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25 Gln Glu Thr His Pro Gln Glu Leu Phe Arg Glu Cys Ser His Tyr Cys
115 120 125

Glu Leu Val Ser Ser Pro Glu Gln Ile Pro Gln Val Leu Ala Ile Ala
130 135 140

30 Met Arg Lys Ala Val Leu Asn Arg Gly Val Ser Val Val Val Leu Pro
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35 Gly Asp Val Ala Leu Lys Pro Ala Pro Glu Gly Ala Thr Met His Trp
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Tyr His Ala Pro Gln Pro Val Val Thr Pro Glu Glu Glu Glu Leu Arg
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40 Lys Leu Ala Gln Leu Leu Arg Tyr Ser Ser Asn Ile Ala Leu Met Cys
195 200 205

Gly Ser Gly Cys Ala Gly Ala His Lys Glu Leu Val Glu Phe Ala Gly
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10076416.01903

Lys Ile Lys Ala Pro Ile Val His Ala Leu Arg Gly Lys Glu His Val
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5 Glu Tyr Asp Asn Pro Tyr Asp Val Gly Met Thr Gly Leu Ile Gly Phe
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Ser Ser Gly Phe His Thr Met Met Asn Ala Asp Thr Leu Val Leu Leu
260 265 270

10 Gly Thr Gln Phe Pro Tyr Arg Ala Phe Tyr Pro Thr Asp Ala Lys Ile
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Ile Gln Ile Asp Ile Asn Pro Ala Ser Ile Gly Ala His Ser Lys Val
15 290 295 300

Asp Met Ala Leu Val Gly Asp Ile Lys Ser Thr Leu Arg Ala Leu Leu
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20 Pro Leu Val Glu Glu Lys Ala Asp Arg Lys Phe Leu Asp Lys Ala Leu
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Glu Asp Tyr Arg Asp Ala Arg Lys Gly Leu Asp Asp Leu Ala Lys Pro
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25 Ser Glu Lys Ala Ile His Pro Gln Tyr Leu Ala Gln Gln Ile Ser His
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Phe Ala Ala Asp Asp Ala Ile Phe Thr Cys Asp Val Gly Thr Pro Thr
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Val Trp Ala Ala Arg Tyr Leu Lys Met Asn Gly Lys Arg Arg Leu Leu
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35 Gly Ser Phe Asn His Gly Ser Met Ala Asn Ala Met Pro Gln Ala Leu
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Gly Ala Gln Ala Thr Glu Pro Glu Arg Gln Val Val Ala Met Cys Gly
420 425 430

40 Asp Gly Gly Phe Ser Met Leu Met Gly Asp Phe Leu Ser Val Val Gln
435 440 445

Met Lys Leu Pro Val Lys Ile Val Val Phe Asn Asn Ser Val Leu Gly
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Phe Val Ala Met Glu Met Lys Ala Gly Gly Tyr Leu Thr Asp Gly Thr
 5 465 470 475 480

Glu Leu His Asp Thr Asn Phe Ala Arg Ile Ala Glu Ala Cys Gly Ile
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10 Thr Gly Ile Arg Val Glu Lys Ala Ser Glu Val Asp Glu Ala Leu Gln
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Arg Ala Phe Ser Ile Asp Gly Pro Val Leu Val Asp Val Val Val Ala
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15 Lys Glu Glu Leu Ala Ile Pro Pro Gln Ile Lys Leu Glu Gln Ala Lys
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 30 <213> *Escherichia coli*

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 35 <223> Mutagenic DNA

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 40 <223> Technical DNA/residues of the polylinker sequence

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15 <222> (1399)..(1454)

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 <212> DNA
 5 <213> *Escherichia coli*

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 10 <223> Start codon of the delta poxB allele

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 <222> (1)..(605)
 15 <223> 5' region of the delta poxB allele

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 <222> (606)..(674)
 20 <223> Technical DNA/residues of the polylinker sequence

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 <222> (675)..(1445)
 25 <223> 3' region of the delta poxB allele

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 <222> (1446)..(1448)
 30 <223> Stop codon of the delta poxB allele

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 35 accatcgagt ggatgtccac ccgccacgaa gaagtggcgg cctttgccgc tggcgctgaa 180
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 taaggtaa 1448

15